

occurring from winter to spring. The population reached maximum densities in May (late spring), when the largest blades were observed, began to decline in June, and had completely disappeared by July.

9D.41

IDENTIFICATION OF THE MATING TYPE LOCUS IN PENNATE DIATOMS

Ives Vanstechelman (ivste@psb.vib-ugent.be), Pieter Vanormelingen (Pieter.Vanormelingen@ugent.be), Wim Vyverman (Wim.Vyverman@ugent.be), Marnik Vuylsteke (mavu@psb.vib-ugent.be) and Koen Sabbe (Koen.Sabbe@ugent.be)

Department of Biology, University of Ghent, Ghent, Belgium

Diatoms have a unique diplontic life cycle characterized by gradual size reduction which ultimately leads to programmed cell death. The latter, which often leads to loss of strains and cultures, can only be avoided by sexual reproduction, which enables cell size restitution via a specialized type of zygote, called the auxospore. This essential link between cell size recovery and sexual reproduction is unique for diatoms. Until now however, not much is known about the molecular basis of sexual reproduction and sex determination in diatoms. Most sexual determination systems are genetically determined by a specific region, the so-called mating type (MT) locus. We are currently identifying the sex determination system of the pennate marine diatom *Seminavis robusta*. An F1 mapping population was made of 2 parental and 116 progeny cultures. AFLP analysis was performed on the mapping population using 54 different primer combinations resulting in 500 AFLP markers. High density linkage maps were constructed using these markers. This resulted in 28 linkage groups. The sex locus was integrated in the linkage maps by including the sex phenotype as a fictive marker. Illumina sequencing was used to identify sequence alterations between a bulk of the + and a bulk of the - mating type strains of the F1 mapping population. The highest differences in allelic counts are currently being mapped on the *Seminavis* genome sequence which will allow identifying and characterizing the mating type locus. This will be followed by a functional characterization of the MT genes by RT-PCR and genetic transformation, and study of the evolution of the selected MT locus genes in related diatom species.

9D.42

SPECIES COMPOSITION, ZONATION AND BIOMASS OF SEaweEDS IN KONGSFJORDEN, SVALBARD - A BASELINE STUDY

Christian Wiencke¹ (christian.wiencke@awi.de), Katharina Zacher¹ (katharina.zacher@awi.de), Haakon Hop² (haakon.hop@npolar.no), Nikolaj A. Kovaltchouk³ (nickkovaltchouk@hotmail.com) and Barbara Vögele⁴ (barbara@akvaplan.niva.no)

¹Alfred Wegener Institute for Polar and Marine Research, D-27515 Bremerhaven, Germany;

²Norwegian Polar Institute, Fram Centre, N-9296 Tromsø, Norway; ³Marine Research Laboratory, Russian Academy of Sciences, St. Petersburg, 199034 Russia and ⁴Akvaplan-niva, N-9296 Tromsø, Norway

Recent predictions indicate that the water temperatures in Fram Strait of the North Atlantic will increase until the end of this century by about 1.5°C in winter and 3.5°C in summer. As temperature is one of the most important factors controlling biogeographic distribution of seaweeds, distributional shifts are an inevitable effect of global warming. Here, we present data (from 1996) on species composition, zonation and biomass of seaweeds from Hansneset, Kongsfjorden on Spitsbergen, Svalbard (78°55'N, 11°56'E). The majority of species (71%) belonged to the Arctic-temperate distribution group, whereas 6% were endemic Arctic species and the remaining 23% were cosmopolitan species distributed from the tropics to the Arctic. The upper sublittoral (3–5 m depth) was characterised by the brown algae *Fucus distichus*, *Pylaiella littoralis*, *Chordaria flagelliformis*, *Saccorhiza dermatodea*, species of the genera *Acrosiphonia* and *Spongomorpha* (green algae) and *Devaleraea ramentacea* (red alga). The dominant species in the mid-sublittoral (5–15 m depth) were the brown algae *Alaria esculenta*, *Laminaria digitata* and *Saccharina latissima*. The red algae *Callophyllis cristata* and the brown algae *Desmarestia viridis*, *Sphacelaria plumosa* and *D. aculeata* occurred as undergrowth species. The lower sublittoral (15–30 m depth) was characterised by the red algae *Phycodrys rubens* and *Ptilota gunneri*. Both species also grew as undergrowth species in the mid-sublittoral. The endemic Arctic brown alga *Laminaria solidungula* was a rare species at our study site; it